

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/469,641DATE: 11/08/95
TIME: 16:57:11

INPUT SET: S7161.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Hu, Jing-Shan
6 Olsen, Henrik S
7 Rosen, Craig A
8
9 (ii) TITLE OF INVENTION: Human Vascular Endothelial Growth Factor
10 3
11
12 (iii) NUMBER OF SEQUENCES: 6
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
16 Stewart & Olstein
17 (B) STREET: 6 Becker Farm Road
18 (C) CITY: Roseland
19 (D) STATE: NJ
20 (E) COUNTRY: USA
21 (F) ZIP: 07068-1739
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: 08/469,641
31 (B) FILING DATE: 06-JUN-1995
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Ferraro, Gregory D
36 (B) REGISTRATION NUMBER: 36,134
37 (C) REFERENCE/DOCKET NUMBER: 325800-463
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 201-994-1700
41 (B) TELEFAX: 201-994-1744
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

ENTERED

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47      (A) LENGTH: 666 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: Not Relevant
50      (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 1..666
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC      48
63      Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
64          1              5              10              15
65
66      CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG      96
67      Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
68          20              25              30
69
70      AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC      144
71      Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
72          35              40              45
73
74      CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC      192
75      Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
76          50              55              60
77
78      AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC      240
79      Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
80          65              70              75              80
81
82      TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC      288
83      Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
84          85              90              95
85
86      CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG      336
87      Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
88          100             105             110
89
90      ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG      384
91      Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
92          115             120             125
93
94      GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC      432
95      Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
96          130             135             140
97
98      CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA CCC TCC      480
99      Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser

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100      145              150              155              160
101
102      CCA GCT GAC ATC ACC CAA TCC CAC TCC AGC CCC AGG CCC CTC TGC CCA      528
103      Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
104              165              170              175
105
106      CGC TGC ACC CAG CAC CAC CAG TGC CCT GAC CCC CGG ACC TGC CGC TGC      576
107      Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
108              180              185              190
109
110      CGC TGT CGA CGC CGC AGC TTC CTC CGT TGT CAA GGG CGG GGC TTA GAG      624
111      Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
112              195              200              205
113
114      CTC AAC CCA GAC ACC TGC AGG TGC CGG AAG CTG CGA AGG TGA      666
115      Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg *
116              210              215              220
117
118
119      (2) INFORMATION FOR SEQ ID NO:2:
120
121          (i) SEQUENCE CHARACTERISTICS:
122              (A) LENGTH: 221 amino acids
123              (B) TYPE: amino acid
124              (D) TOPOLOGY: linear
125
126          (ii) MOLECULE TYPE: protein
127
128          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
129
130      Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val
131          1              5              10              15
132
133      Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg
134              20              25              30
135
136      Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro
137              35              40              45
138
139      Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala
140              50              55              60
141
142      Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys
143              65              70              75              80
144
145      Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val
146              85              90              95
147
148      Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu
149              100              105              110
150
151      Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys
152              115              120              125

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153
154 Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro
155 130 135 140
156
157 Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser
158 145 150 155 160
159
160 Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro
161 165 170 175
162
163 Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys
164 180 185 190
165
166 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
167 195 200 205
168
169 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
170 210 215 220
171

172 (2) INFORMATION FOR SEQ ID NO:3:

173
174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 29 base pairs
176 (B) TYPE: nucleic acid
177 (C) STRANDEDNESS: Not Relevant
178 (D) TOPOLOGY: linear
179

180 (ii) MOLECULE TYPE: DNA (genomic)
181
182
183
184

185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

186
187 GCATGGATCC CAGCCTGATG CCCCTGGCC
188

29

189 (2) INFORMATION FOR SEQ ID NO:4:

190
191 (i) SEQUENCE CHARACTERISTICS:
192 (A) LENGTH: 30 base pairs
193 (B) TYPE: nucleic acid
194 (C) STRANDEDNESS: Not Relevant
195 (D) TOPOLOGY: linear
196

197 (ii) MOLECULE TYPE: DNA (genomic)
198
199
200
201

202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

203
204 GCATTCTAGA CCCTGCTGAG TCTGAAAAGC
205

30

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206 (2) INFORMATION FOR SEQ ID NO:5:

207

208 (i) SEQUENCE CHARACTERISTICS:

209 (A) LENGTH: 29 base pairs

210 (B) TYPE: nucleic acid

211 (C) STRANDEDNESS: Not Relevant

212 (D) TOPOLOGY: linear

213

214 (ii) MOLECULE TYPE: DNA (genomic)

215

216

217

218

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

220

221 GACTGCATGC ACCAGAGGAA AGTGGTGTC

29

222

223 (2) INFORMATION FOR SEQ ID NO:6:

224

225 (i) SEQUENCE CHARACTERISTICS:

226 (A) LENGTH: 29 base pairs

227 (B) TYPE: nucleic acid

228 (C) STRANDEDNESS: Not Relevant

229 (D) TOPOLOGY: linear

230

231 (ii) MOLECULE TYPE: DNA (genomic)

232

233

234

235

236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

237

238 GACTAGATCT CCTTCGCAGC TTCCGGCAC

29

239

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/469,641

DATE: 11/08/95
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Line	Error	Original Text
169	Stop Codon at end of sequence removed - no error	